Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (previously presented) A microarray comprising a plurality of features, each of the features formed of single stranded oligonucleotides constructed on and arranged on a common planar substrate, each of the features including in the same feature two different oligonucleotides, the different oligonucleotides being different in nucleotide sequence from each other.

2. (original) A microarray as claimed in claim 1 wherein each feature includes oligonucleotides of two different sequences.

3. (previously presented) A microarray comprising a plurality of features, each of the features formed of single stranded oligonucleotides constructed on and arranged on a common planar substrate, each of the features including in the same feature two different oligonucleotides, the oligonucleotides being different in nucleotide sequence from each other, wherein at least some of the oligonucleotides in the microarray are oriented both 3' to 5' and at least some other oligonucleotides are oriented 5' to 3'.

4. (previously presented) A microarray comprising a plurality of features, each of the features formed of single stranded oligonucleotides constructed on and arranged on a common planar substrate, each of the features including in the same feature two different oligonucleotides, the oligonucleotides being different in nucleotide sequence from each other, wherein the two oligonucleotides in a single feature are each designed to hybridize to different exons in the same eukaryotic gene.

5. (previously presented) A microarray as claimed in claim 1 wherein the two oligonucleotides each make up about 50% of the oligonucleotides in the feature.

6. (withdrawn) A method for synthesizing different oligonucleotides in the same feature area, the method comprising the steps of:

providing a substrate for manufacturing a microarray, the substrate having photo-labile

protecting groups formed on its surface, the microarray having at least one feature area;

exposing the feature area to a light source for a period of time sufficient to cleave the photo-labile protecting group from only a portion of feature area;

coupling a second protecting group to the unprotected area of the feature, the second protective group not being photo-labile;

exposing the feature area to a light source for a period of time to cleave the remaining photo-labile protecting groups from the feature area to leave an unprotected area of the feature;

building a first group of oligonucleotides in the unprotected area of the feature;

capping the first group of oligonucleotides with a capping compound that is not photo-labile;

removing the second protecting group from the feature area to leave an unprotected area of the feature;

building a second group of oligonucleotides in the unprotected area of the feature.

7. (withdrawn) The method of Claim 6 wherein the portion of the feature area in which the first light exposing step is conducted is about 50% of the feature area, so that each of the oligonucleotides is about 50% of the oligonucleotides in the feature.

8. (withdrawn) The method of Claim 6 wherein the portion of the feature area in which the first light exposing step is conducted is about 33% of the feature area, so that one of the oligonucleotides is about 33% of the oligonucleotides in the feature..

9. (withdrawn) The method of Claim 6 wherein the second protecting group is acid labile.

10. (withdrawn) The method of Claim 9 wherein the second protective group is di-methoxy-trityl

11. (withdrawn) The method of Claim 9 wherein the capping compound is acetic anhydride and tetrahydrofuran.

12. (withdrawn) A method of using a microarray to analyze the splicing of an mRNA transcript from a gene having more than one exon, the method incorporating the steps of

providing a microarray with at least one feature two oligonucleotides in the feature, a first oligonucleotide being complementary to the mRNA in a portion of the mRNA corresponding to one exon and a second oligonucleotide corresponding in sequence to the mRNA in a portion corresponding to another exon;

hybridizing the microarray to the mRNA so that mRNA if present will bind to the nucleotide complementary to the mRNA;

extending the first oligonucleotide using the bound mRNA as a template;

removing the bound mRNA;

hybridizing the extended first oligonucleotide to the second oligonucleotide; and

extending the second oligonucleotide against first oligonucleotide using labeled nucleotides so that the feature can be detected if the hybridizations occurred.